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Full Record**Details for HUGENEFL:M12625_AT****Full Screen**
NetAffx Links [Cluster Members](#)
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GeneChip Array Information
Probe Set ID M12625_at
**GeneChip
Array** HumanGeneFL Array
**Organism
Common
Name** Human
Probe Design Information
Transcript ID M12625
**Sequence
Type** Exemplar sequence
**Representative
Public ID** M12625 [NCBI](#)
**Target
Description** M12625, class B, 20 probes, 13 in M12625mRNA 893-1259: 7 in reverseSequence, 1599-1683, Human lecithin-cholesterol acyltransferase mRNA, complete cds, with 5' and 3' flanking DNA sequences
Genomic Alignment of Target Sequence
Assembly April 2003 (NCBI 33)
Alignment(s)

	Position	% Identity	Cytoband
chr16: 67749925-67750484 (-)	UCSC	100	q22.1

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	M12625 NCBI	lecithin-cholesterol acyltransferase	chr16:67749888-67754507 (-) UCSC

Public Domain and Genome References
Gene Title lecithin-cholesterol acyltransferase
Gene Symbol LCAT [HGNC](#)
**Chromosomal
Location** 16q22.1
UniGene ID Hs.387239 [NCBI](#) (FULL LENGTH)
Ensembl ENSG00000103080 [Ensembl](#)
LocusLink 3931 [NCBI](#)
SwissProt AAP88750 [EMBL-EBI](#)
P04180 [EMBL-EBI](#)
EC 2.3.1.43
OMIM 606967 [NCBI](#)

RefSeq Protein ID NP_000220 [NCBI](#)

RefSeq RefSeq Transcript ID RefSeq Title
NM_000229 [NCBI](#) lecithin-cholesterol acyltransferase precursor

Functional Annotations

	ID	Title	Organism	Type
Ortholog	MG-U74AV2:103023_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	MG-U74AV2:161759_R_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	MOE430A:1417043_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	MU11KSUBA:J05154_S_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	RAE230A:1367887_AT	lecithin cholesterol acyltransferase	Rat	Curated Ortholog
	RG-U34A:X54096_AT	lecithin cholesterol acyltransferase	Rat	Curated Ortholog
	MOUSE430_2:1417043_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	MOUSE430A_2:1417043_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
6629	lipid metabolism	inferred from electronic annotation	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5576	extracellular	not recorded	QuickGO AmiGO

Gene Ontology

GO Molecular Function (view graph)

ID	Description	Evidence	Links
4607	phosphatidylcholine-sterol O-acyltransferase activity	inferred from electronic annotation	QuickGO AmiGO
8415	acyltransferase activity	inferred from electronic annotation	QuickGO AmiGO
16740	transferase activity	inferred from electronic annotation	QuickGO AmiGO

	Method	ID	Description	E-Value
Protein Similarities	blast	32879837		0.0
	blast	4557892	lecithin-cholesterol acyltransferase precursor [Homo sapiens]	0.0

	Method	ID	Description	E-Value
Protein Families	ec	LCAT_HUMAN	LCAT_HUMAN	1.85E-171
			EC:2.3.1.43:PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE).	

Database	ID	Description	E-Value
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scop d1tca__ d1tca__ SCOP:c.69.1.17:| Triacylglycerol lipase 5.3E-8
 pfam LACT Lecithin:cholesterol acyltransferase 1.7E-182

InterPro IPR003386 Lecithin:cholesterol acyltransferase
EMBL-EBI

Protein Domains

InterPro IPR008262 Lipase, active site
EMBL-EBI

Trans Membrane

ID	Number Of Domains	Probability of Interior N-Terminus
NP_000220	2	0.05945

Sequence

>HUGENEFL:M12625_AT

cttcaactacacaggccgtgacttccaacgcttctttgcagacctgcactttgaggaagg
 ctggtacatgtggctgcagtcacgtgacctcctggcaggactcccagcacctgggtgtgga
 agtatactgtctttacggcgtgggctgcccacgccccgcacctacatctacgaccacgg
 cttcccctacacggacctgtgggtgtgctctatgaggatgggtgatgacacgggtggcgac
 ccgcagcaccgagctctgtggcctgtggcagggccgcccagccacagcctgtgcacctgtc
 gcccctgcacgggatacagcatctcaacatgggtcttcagcaacctgacctggagcacat
 caatgccatcctgctgggtgcctaccgcccagggtccccctgcacccccgactgccagccc
 agagcccccgccctcctgaataaagaccttcccttgctaccgtaagccctgatggctatgt
 ttcaggttgaagggaggcactagagtcccacactaggtttcactcctcaccagccacagg
 ctgagtgctgtgtgcagtg

Target Sequence

Probe Info	Probe Sequence(5'-3')	Probe		Probe Interrogation Position	Strandedness
		X	Y		
	CTTCAACTACACAGGCCGTGACTTC	152	127	1161	Antisense
	CTACACAGGCCGTGACTTCCAACGC	153	127	1167	Antisense
	CCAACGCTTCTTTGCAGACCTGCAC	154	127	1185	Antisense
	CCTGCACTTTGAGGAAGGCTGGTAC	155	127	1203	Antisense
	CATGTGGCTGCAGTCACGTGACCTC	156	127	1227	Antisense
	GCTGCAGTCACGTGACCTCCTGGCA	157	127	1233	Antisense
	CCTGGCAGGACTCCCAGCACCTGGT	158	127	1251	Antisense
	GGACCCTGTGGGTGTGCTCTATGAG	159	127	1353	Antisense
	TGTGCTCTATGAGGATGGTGATGAC	160	127	1365	Antisense
	GGCGACCCGCAGCACCGAGCTCTGT	161	127	1395	Antisense
	CCTGACCCTGGAGCACATCAATGCC	162	127	1503	Antisense
	GCACATCAATGCCATCCTGCTGGGT	163	127	1515	Antisense
	CATCCTGCTGGGTGCCTACCGCCAG	164	127	1527	Antisense
	CTTTGCTACCGTAAGCCCTGATGGC	165	127	1611	Antisense
	TACCGTAAGCCCTGATGGCTATGTT	166	127	1617	Antisense
	AAGCCCTGATGGCTATGTTTCAGGT	167	127	1623	Antisense
	CTATGTTTCAGGTTGAAGGGAGGCA	168	127	1635	Antisense
	GGAGGCACTAGAGTCCCACACTAGG	169	127	1653	Antisense
	GTCCCACACTAGGTTTCACTCCTCA	170	127	1665	Antisense
	CACAGGCTCAGTGCTGTGTGCAGTG	171	127	1695	Antisense

